What Might have been the Ancestor of New World Siskins?

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Abstract: Eurasian Carduelis spinus (siskin) has given rise to the C.pinus (pine siskin) North American radiation, which includes C.dominicensis, C.p. perplexus and C.atriceps. It is addressed the question why C.spinus is not thriving now in America.

INTRODUCTION

The Eurasian Siskin (Carduelis spinus) appeared on Earth in the Pliocene Epoch about five million years ago (MYA) [1, 2]. It is the one extant direct ancestor of several North American finches (see Fig. 1 inset), which appeared after 2 MYA [1, 2], which are named as follows:

1. Carduelis dominicensis, the Antillean Siskin from the Caribbean high peaks of La Hispaniola Island.
2. Carduelis pinus pinus, the Pine Siskin from North America.
3. Carduelis pinus perplexus, the Pine Siskin from Guatemalan altiplano.
4. Carduelis atriceps, the Black-capped Siskin from Guatemalan altiplano.

RESULTS & DISCUSSION

Nowadays, the Eurasian Siskin does not thrive in America, but in easternmost and westernmost Eurasia, having a gap between Central Russia and its easternmost range. The most important feature of the Eurasian Siskin is that it is a migratory bird whose North to South migrations do not always follow the same longitudinal patterns (“irruptive”) [3]. It is feasible that Carduelis spinus was thriving in Eurasia and also in North America around the Pliocene / Pleistocene Epoch limit, about 2 MYA. Soon after this time, the first glaciation covered North America with a kilometric thick ice shield [4]. The Eurasian Siskin might have taken refuge in ice-free Caribbean Islands and in Mexican Mountains and Guatemalan-Mexican altiplano. Its Summer-Winter and North-South migrations would have been disrupted because it became isolated in all-year relatively warm temperature (Caribbean); year-round relatively and quite stable low temperature (Guatemalan-Mexican altiplano) and relatively temperature stable Mexican Mountains. The Eurasian Siskin could have first given rise to the endemic Antillean Siskin (Carduelis dominicensis) at the Caribbean high peaks of La Hispaniola Island soon after 2 MYA (Fig. 1) [5]. Afterward, about 200,000 years ago, the Eurasian Siskin might have given rise to the Pine Siskin Carduelis pinus pinus in the non-glaciated Mexican Sierras [4]; at about the same time (200,000 years ago), the Black-capped Siskin (Carduelis atriceps) and the Pine Siskin Carduelis pinus perplexus might have appeared in the non-glaciated Guatemalan-Mexican altiplano [4]. Rainfall variations in the Caribbean during the Pleistocene, however, could have also affected the distribution of these birds [6].

This would be a typical example of adaptive radiation caused by a North to South migration barrier (First North American Ice Shield Glaciation) and provincialism that drove evolution to create these new finches species. When last Wisconsin Glaciation ended and North American ice melted about 12,000 years ago, Carduelis pinus would have followed the ancestral North to South migrations and covered all North America, occupying the American niches that the Eurasian Siskin couldn’t reach from Asia during the last 2 million years because of the extant thick ice shield; neither could it afterwards because of species competition by ecologic niche with its descent Carduelis pinus. This evolutionary theory for the finch group appearance is schematic. More complicated events may have occurred during the Nebraskan, Kansan, Illinoan and Wisconsin North American glaciations, and / or their respective interglacial periods (Aftonian, Yarmouth and Sangamon) [4], and other explanations may also be possible, see [7].

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REFERENCES

Fig. (1). The Eurasian Siskin (*Carduelis spinus*) possibly thrived in North America before two million years ago when glaciations started. The ice shield on North America could have driven speciation by provincialism of ‘daughter species’ isolated in the Caribbean Mountains (*C. dominicensis*), in Mexican Sierras (*C. p. pinus*) and in Mexican-Guatemalan altiplano (*C. p. perplexus* and *C. a. atriceps*). See also ref. [2]. Present day ranges: *C. p. pinus* in yellow; *C. dominicensis* in red; *C. atriceps* in orange; *C. p. perplexus* in purple. Inset represents a Bayesian Inference dendrogram based on mitochondrial cytochrome b DNA sequences. Note that the nodes are strongly supported, like in previous works [2] which used other methodologies.


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